

Statistical Inference

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Statistical Inference

Natural phenotypic variation within a species or population is largely quantitative, polygenic, and controlled by the interaction of environmental and genetic factors. A major goal of any phenotype to genotype linkage is to be able to rapidly identify and predict the causal genetic variation underlying the phenotypic variation. Advances in this area could greatly facilitate diverse scientific fields from ecology to breeding to medicine. Current technological advances in phenotyping and genotyping are allowing increasingly rapid advances in determining the genetic architecture underlying diverse phenotypes. However both genomics and phenotyping systems have begun to generate vastly more data than can be easily interrogated on local systems or by non-expert laboratories. As such, this working group will be working to develop a platform that can make advanced computational approaches to statistically link genotype to phenotype more available to the general user and more rapid for the specialist user.

Currently there are largely two approaches geared towards mapping genetic loci controlling polymorphism using transcriptomics, metabolomics and enzymatic platforms. These data have frequently been used in structured mapping populations and more recently this is being expanded to the complementary approach of genome wide association mapping. Both approaches have been focused on identifying associations between phenotypes and genotypes, at a genome-wide level. In the future with the advent of whole genome genotyping, the computational discrepancies between the analysis of structured and non-structured populations will begin to disappear potentially allowing the data to be analyzed on a common platform.